

SEQUENCE LISTING

<110> Unilever PLC  
Unilever N.V.  
FRENKEN, Leo G. J.  
HOWELL, Steven  
VAN DER VAART, Jan M.

<120> Antigen-Binding Proteins

<130> 56159-5041

<140> US 09/807,172

<141> 2001-04-10

<150> PCT/EP98/06991

<151> 1998-10-27

<150> EP 99303118.6

<151> 1999-04-22

<150> PCT/EP99/08323

<151> 1999-10-22

<160> 51

<170> PatentIn version 3.1

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Gly Thr Ser Gly Ser  
1 5

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Ser Ser Ser Ala Ser Ala Ser Ser Ala  
1 5

<210> 3



<220>

<223> Primer

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aacagttaag cttccgcttg cggccgcgga gctggggctct tcgctgtggt gcg 53

<210> 8

<211> 53

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aacagttaag cttccgcttg cggccgctgg ttgtggtttt ggtgtcttgg gtt 53

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gggaattcca ataggtgggt agcaatcg 28

<210> 10

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gaccaacgtg gtcgcctggc aaaacg 26

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cgttttgccg ggcgaccacg ttggtc 26

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Gln Val Gln Leu Gln  
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tggttggttt tgcagccaaa atatctgcgc aggtgcagct gcaggagtca taatgagggg 120
cccaggtcac cgtctcctca gaacaaaaac tcatctcaga agaggatctg aattaatgac 180
ttaagctt                                     188
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Ala His His Thr Asn Lys Gln Asn Lys Met Met Leu Leu Gln Ala Phe  
1 5 10 15

Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys Ile Ser Ala Gln Val Gln  
20 25 30

Leu Gln Glu Ser



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ttc atg ggc tgg tac cgc cag gct cca ggg aag cag cgc gag ttg gtc      144
Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
      35                      40                      45

gca acc att aat agt aga ggt atc aca aac tat gca gac ttc gtg aag      192
Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
      50                      55                      60

ggc cga ttc acc atc tcc aga gac aat gcc aag aag aca gtg tat ttg      240
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
      65                      70                      75                      80

gaa atg aac agc ctg gaa cct gaa gac acg gcc gtt tat tac tgt tac      288
Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
      85                      90                      95

act cac tac ttc aga tcc tac tgg ggt cag ggg acc cag gtc acc gtc      336
Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
      100                      105                      110

tcc tca
Ser Ser
      342

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<210> 22  
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<400> 22

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Glu
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Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly Gly
      20                      25                      30

Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
      35                      40                      45

Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val Lys
      50                      55                      60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu
      65                      70                      75                      80

Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Tyr
      85                      90                      95

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Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val  
100 105 110

Ser Ser

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Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr  
 20 25 30

Asp Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val  
 35 40 45

Ala Ala Ile Asn Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val  
 50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys  
 85 90 95

Gly Ala Gly Glu Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln  
 100 105 110

Val Thr Val Ser Ser  
 115

<210> 25  
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<400> 25  
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43

<210> 26  
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<213> Artificial sequence

<220>

<223> Primer

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ccctgggtcc agtggcagag gagtggcaga ggagtcttgt tt

42

<210> 27

<211> 24

<212> DNA

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<220>

<223> Primer

<400> 27

caggtccagc tgcaggagtc tggg

24

<210> 28

<211> 24

<212> DNA

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<223> Primer

<400> 28

caggtgaaac tgctcgagtc wggg

24

<210> 29

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<212> DNA

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<223> Linker; Double stranded

<220>

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<222> (2)..(40)

<223>

<400> 29

g gtc acc gtc tcc tca cag gtg cag ctg cag gag tca ctg taatgactta

50

Val Thr Val Ser Ser Gln Val Gln Leu Gln Glu Ser Leu

1

5

10

agctt

55

<210> 30

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0961 3720 ... 077 6720

<223> Linker; Double stranded

Val Thr Val Ser Ser Gln Val Gln Leu Gln Glu Ser Leu

<210> 31

<211> 8

<212> PRT

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 $\langle 220 \rangle$ 

<223> Primer

<400> 31

Gln Val Gln Leu Gln Glu Ser Gly

1 5

<210> 32

<211> 672

<212> DNA

<213> Artificial sequence

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<223> Plasmid Construct

 $\langle 220 \rangle$ 

&lt;221&gt; CDS

<222> (1) .. (672)

$\langle 223 \rangle$

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ctc gag tca ggg gga gga ttg gtg cag gcg ggg ggc tct ctg aga ctc 48  
Leu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu  
1 5 10 15

tcc tgt gca gcc tct gga cgc acc ggc agt acg tat gac atg ggc tgg 96  
Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp  
20 25 30

ttc cgc cag gct cca ggg aag gag cgt gag tct gta gca gct att aac 144  
 Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn  
 35 40 45

tgg	gat	agt	gcg	cgc	aca	tac	tat	gca	agc	tcc	gtg	agg	ggc	cga	ttc		192
Trp	Asp	Ser	Ala	Arg	Thr	Tyr	Tyr	Ala	Ser	Ser	Val	Arg	Gly	Arg	Phe		
	50					55					60						

acc atc tcc aga gac aac gcc aag aag acg gtg tat ctg caa atg aac 240  
Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn

65				70				75				80				
agc	ctg	aaa	cct	gag	gac	acg	gcc	ggt	tat	acc	tgt	ggc	gcg	ggg	gaa	288
Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Thr	Cys	Gly	Ala	Gly	Glu	
				85					90					95		
ggg	ggg	act	tgg	gac	tcc	tgg	ggc	cag	ggg	acc	cag	gtc	acc	gtc	tcc	336
Gly	Gly	Thr	Trp	Asp	Ser	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	
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tca	cag	gtg	cag	ctg	cag	gag	tca	ggg	gga	ggc	ttg	gtg	cag	gct	ggg	384
Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	
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gag	tct	ctg	aaa	ctc	tcc	tgt	gca	gcc	tct	gga	aac	acc	ttc	agt	ggc	432
Glu	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Asn	Thr	Phe	Ser	Gly	
				130					135					140		
ggc	ttc	atg	ggc	tgg	tac	cgc	cag	gct	cca	ggg	aag	cag	cgc	gag	ttg	480
Gly	Phe	Met	Gly	Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	
				145					150					155	160	
gtc	gca	acc	att	aat	agt	aga	ggt	atc	aca	aac	tat	gca	gac	ttc	gtg	528
Val	Ala	Thr	Ile	Asn	Ser	Arg	Gly	Ile	Thr	Asn	Tyr	Ala	Asp	Phe	Val	
				165					170					175		
aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	aat	gcc	aag	aag	aca	gtg	tat	576
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Lys	Thr	Val	Tyr	
				180					185					190		
ttg	gaa	atg	aac	agc	ctg	gaa	cct	gaa	gac	acg	gcc	gtt	tat	tac	tgt	624
Leu	Glu	Met	Asn	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				195					200					205		
tac	act	cac	tac	ttc	aga	tcc	tac	tgg	ggt	cag	ggg	acc	cag	gtc	acc	672
Tyr	Thr	His	Tyr	Phe	Arg	Ser	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	
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<210> 33
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<220>  
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<400> 33

Leu Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly Ser Leu Arg Leu  
1 5 10 15

Ser Cys Ala Ala Ser Gly Arg Thr Gly Ser Thr Tyr Asp Met Gly Trp  
20 25 30

Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Ser Val Ala Ala Ile Asn  
 35 40 45

Trp Asp Ser Ala Arg Thr Tyr Tyr Ala Ser Ser Val Arg Gly Arg Phe  
 50 55 60

Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr Leu Gln Met Asn  
 65 70 75 80

Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Thr Cys Gly Ala Gly Glu  
 85 90 95

Gly Gly Thr Trp Asp Ser Trp Gly Gln Gly Thr Gln Val Thr Val Ser  
 100 105 110

Ser Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly  
 115 120 125

Glu Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Asn Thr Phe Ser Gly  
 130 135 140

Gly Phe Met Gly Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu  
 145 150 155 160

Val Ala Thr Ile Asn Ser Arg Gly Ile Thr Asn Tyr Ala Asp Phe Val  
 165 170 175

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Lys Thr Val Tyr  
 180 185 190

Leu Glu Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys  
 195 200 205

Tyr Thr His Tyr Phe Arg Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr  
 210 215 220

<210> 34  
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<400> 34

gtcacgtct ctatgggcc accaggtgca gctgcaggag tcaactta

48

<210> 35  
 <211> 47  
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<220>  
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<400> 35  
 gcagagatct accggtgggc cagtcgagc tcctcagttg aattcga

47

<210> 36  
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<220>  
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<400> 36  
 ctatgggtac ttccggttcc cag

23

<210> 37  
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<220>  
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<400> 37  
 accatgaagg ccaagg

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<210> 38  
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<400> 38  
 ctatgtcttc atctgcttct gcctcttcag ccag

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<210> 39  
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<400> 39

aagaagtaga cgaagacgga gaagtcgg

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ctagtggttc tccaggttca ccaggtcag

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<400> 41

accaagaggt ccaagtggtc ca

22

<210> 42

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<212> DNA

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ctagtgtac tacaactggt tcttcaccag gtccaactca g

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acgatgatgt tgaccaagaa gtggtccagg ttga

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32

<210> 45

<211> 25

<212> DNA

<213> Artificial sequence

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<223> Linker

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acgattagta agaccattac gaaga

25

<210> 46

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<213> Artificial sequence

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<223> Primer

<400> 46

Gln Val Lys Leu Leu Glu Ser Gly

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5

<210> 47

<211> 7

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Ser Gly Thr Ser Gly Ser Gln

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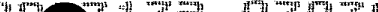
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